5.0 and GAP extension penalty of 0.3, and is capable of initiating replication; and (2) replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS; and

(ii) a polynucleotide sequence of interest, wherein there are vectors in the population that vary from other vectors in the population by carrying different versions of the polynucleotide sequence of interest;

(b) cultivating the cells in the presence of an effective amount of a selective agent or the absence of an appropriate selective agent;

(c) selecting or screening for one or more transformants expressing a desired characteristic; and

(d) isolating the transformant(s) of interest.

C1

13. (Twice Amended) The method of claim 1, wherein the replication initiating polynucleotide sequence has at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3.

C2

14. (Twice Amended.) The method of claim 1, wherein the replication initiating polynucleotide sequence is obtained from a filamentous fungal cell.

C3

17. (Twice amended.) The method of claim 1, wherein the replication initiating polynucleotide sequence has the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2.

C4

30. (Amended.) The method of claim 1, wherein the polynucleotide sequence of interest is a control sequence.

Please add the following new claims:

Sub P3

C5

31. (New) A method of constructing a library of polynucleotide sequences of interest in filamentous fungal cells, wherein the method comprises:

(a) transforming the fungal cells with a population of DNA vectors, wherein each vector comprises:

(i) a fungal selection marker polynucleotide sequence and a fungal replication initiating polynucleotide sequence, wherein the marker and the replication initiating sequence do not vary within the population; and wherein the replication initiating sequence is a nucleic acid sequence selected from the group consisting of: (1) a replication initiating sequence having at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3, and is capable of initiating replication; and (2) replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS; and

(ii) a polynucleotide sequence of interest, wherein there are vectors in the population that vary from other vectors in the population by carrying different versions of the polynucleotide sequence of interest;

(b) cultivating the cells in the presence of an effective amount of a selective agent or the absence of an appropriate selective agent.

32. (New.) The method of claim 31, further comprising the steps of:

(c) selecting or screening for one or more transformants expressing a desired characteristic; and

(d) isolating the transformant(s) of interest.